

Amendments To The Claims

Claim 1 (currently amended) A method of determining whether a sample includes at least one analyte of interest, said method comprising:

- (a) contacting said sample with ~~an~~ a planar array of a plurality of distinct binding agents displayed on a surface of a solid support, wherein each of said binding agents at least comprises a specific epitope binding domain of an antibody;
- (b) detecting the presence of any resultant binding complexes on said surface to obtain analyte binding data; and
- (c) employing said analyte binding data to determine whether said sample includes said at least one analyte of interest;

wherein said method provides a sensitivity of at least 10pg/ml of analyte of interest when said analyte is directly fluorescently labeled.

Claim 2 (original): The method according to Claim 1, wherein said sample is contacted with said array in the presence of a metal ion chelating polysaccharide.

Claim 3 (original): The method according to Claim 2, wherein said metal ion chelating polysaccharide comprises polygalactouronate domains.

Claim 4 (original): The method according to Claim 3, wherein said metal ion chelating polysaccharide is a pectin.

Claim 5 (original): The method according to Claim 4, wherein said pectin is apple pectin.

Claim 6 (original): The method according to Claim 1, wherein said method further comprises extracting said at least one analyte from a cellular source and labeling said extracted at least one analyte, wherein said extracting and labeling steps employ the same buffer composition.

Claim 7 (original): The method according to Claim 6, wherein said buffer composition is free of components that include primary amine moieties.

Claim 8 (original): The method according to Claim 7, wherein said buffer composition has a pH ranging from about 7 to about 12.

Claim 9 (original): The method according to Claim 8, wherein said buffer composition is capable of extracting at least about 95% of the proteins of an initial cellular source.

Claim 10 (original): The method according to Claim 1, wherein said at least one analyte is a protein.

Claim 11 (original): The method according to Claim 1, wherein said method comprises determining the presence of at least two distinct analytes in said sample.

Claim 12 (original): The method according to Claim 1, wherein said method comprises a plurality of washing steps between said contacting and detecting steps.

Claim 13 (original): The method according to Claim 1, wherein: (a) said method comprises quantitatively detecting at least two different protein analytes in said sample; (b) said sample is contacted with said array in the presence of a metal ion chelating polysaccharide; (c) said method further comprises extracting said at least one analyte from a cellular source and labeling said extracted at least one analyte, wherein said extracting and labeling steps employ the same buffer composition; and (d) wherein said method comprises a plurality of washing steps between said contacting and detecting steps.

Claim 14 (original): The method according to Claim 13, wherein said metal ion chelating polysaccharide comprises polygalactouronate domains.

Claim 15 (original): The method according to Claim 14, wherein said metal ion chelating polysaccharide is a pectin.

Claim 16 (original): The method according to Claim 15, wherein said pectin is apple pectin.

Claim 17 (original): The method according to Claim 13, wherein said method is a method of determining a protein expression profile for said sample.

Claim 18 (original): The method according to Claim 1, wherein said method further comprises a sample fractionating step prior to said contacting step.

Claim 19 (original): The method according to Claim 18, wherein said fractionating step comprises contacting said sample with at least one affinity column.

Claim 20-44 (withdrawn)